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SEQUENCE LISTING

<110> SUNTORY LIMITED

<120> A gene encoding an enzyme for catalyzing biosynthesis of lignan,  
and use thereof

<130> SU0411

<140> PCT/JP2004/0146696

<141> 2004-09-24

<150> JP 2003-341313

<151> 2003-09-30

<150> JP 2003-432383

<151> 2003-12-26

<160> 79

<170> PatentIn Ver. 2.1

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Val	Ala	Ala	Lys	Arg	Tyr	Tyr	Gly	Glu	Glu	Ala	Glu	Asp	Asp	Glu	Glu	195	200	205	
Ala	Lys	Arg	Phe	Arg	Asp	Leu	Thr	Lys	Glu	Ala	Leu	Glu	Leu	Thr	Ser	210	215	220	
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<210> 12  
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<210> 13

<211> 24

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<223> SiP249

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Met	Ser	Ile	Pro	Leu	Leu	Ile	Ser	Leu	Ser	Leu	Ile	Ile	Leu	Val	Phe
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			20					25					30		
Arg	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Pro	Phe	Leu	Gly	Asn	Leu	Leu	Gln
			35				40					45			
Tyr	Asn	Pro	Ser	Asp	Leu	His	Leu	Arg	Leu	Thr	Lys	Leu	Ser	Glu	Lys
	50					55					60				
Tyr	Gly	Pro	Leu	Met	Tyr	Met	Thr	Phe	Val	Gly	Lys	Pro	Val	Val	Val
65					70					75					80
Ile	Ser	Ser	Ala	Arg	Val	Ala	Lys	Glu	Ala	Leu	Lys	Tyr	Asn	Asp	Leu
				85					90					95	
Ala	Phe	Ser	Ser	Arg	Pro	Ser	Thr	Ile	Ala	Ser	Arg	Lys	Val	Ala	Tyr
			100					105					110		
Asn	Asn	Ser	Asp	Ile	Ser	Met	Ser	Pro	Tyr	Thr	Glu	Tyr	Trp	Arg	Glu
	115						120					125			
Leu	Arg	Lys	Met	Val	Val	Leu	Arg	Leu	Phe	Thr	Val	Lys	Gln	Val	Asn
	130					135					140				
Ser	Phe	Arg	Pro	Ala	Arg	Glu	Glu	Glu	Val	Ala	Arg	Met	Val	Lys	Glu
145					150					155					160
Ile	Ser	Arg	Arg	Ala	Asn	Ala	His	Gln	Pro	Val	Asn	Ile	Asn	Glu	Ile
				165					170					175	
Ala	Leu	Ser	Leu	Ser	Ser	Arg	Met	Ile	Ser	Arg	Phe	Ala	Leu	Gly	Lys
			180					185					190		
Arg	Tyr	Asp	Glu	Glu	Asn	Gly	Pro	Glu	Lys	Arg	Arg	Phe	Asp	Arg	Ile
		195					200					205			
Leu	Gln	Leu	Leu	Gln	Leu	Val	Ser	Val	Glu	Ile	Phe	Phe	Gly	Asp	Tyr
	210					215					220				
Ser	Pro	Trp	Leu	Gly	Trp	Ile	Asp	Arg	Leu	Cys	Gly	Lys	Val	Ser	Gln
225					230					235					240
Leu	Glu	Lys	Ala	Phe	Lys	Asp	Leu	Asp	Ser	Leu	Tyr	Glu	Glu	Met	Ile
				245					250					255	
Ala	Glu	His	Leu	Ser	Pro	Asn	Arg	Pro	Glu	Ser	Met	Asn	Gly	Asp	Ile
			260					265					270		

Leu Asp Met Leu Ile Gln Met Lys Glu Asp Arg Ser Ser Thr Val Gln  
 275 280 285  
 Ile Asp Trp Asp His Ile Lys Gly Val Leu Met Asn Met Phe Val Ala  
 290 295 300  
 Gly Thr Asp Thr Thr Ala Ala Thr Ile Thr Trp Ala Met Thr Ala Leu  
 305 310 315 320  
 Ile Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu Ile Arg Ser  
 325 330 335  
 Val Val Gly Lys Lys Gly Ser Val Ala Glu Asp Asp Ile Gln Lys Leu  
 340 345 350  
 Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro  
 355 360 365  
 Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp  
 370 375 380  
 Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala  
 385 390 395 400  
 Ile Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro  
 405 410 415  
 Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly  
 420 425 430  
 Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu  
 435 440 445  
 Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe  
 450 455 460  
 His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp  
 465 470 475 480  
 Phe Leu Pro Gly Ile Thr Thr His Lys Lys Asn Ala Leu Tyr Leu Met  
 485 490 495  
 Ala Lys Ser Tyr Leu  
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<210> 55

<211> 1545

<212> DNA

<213> Sesamum indicum

<220>

<223> SiP288

<400> 55

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cttctgcttc acgtgagccg gattcacgac aattgcacgg agattatggg gaagtcccg 180
cggggaactt ttcatttccg ggggtccctgg ttggctgata tggacatgat ggggactgct 240
gatcctgaga atgttccacta cattatgagc gcgaacttcc agaatttccc gaaaggcccc 300
aagttcaggg aaatttttga tgttcttgga gatgggattt tcaatgcaga ttcggagtcc 360
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ctggcgaaaga tcagccgtga gaaggtagag aaaggcctga ttccagttct tgaaacgggtg 480
tgcctggaaa atcgggtggg cgatttgagc gatttgttcc agagggtgac gtttgataca 540
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cctttctcga aagccctaga tgatgccgaa gaagcgatat tcatgcgcca tgtgggttct 660
gaaaagattt ggaaacttca gaggtgggtt ggggttgat ctgagagaaa attgagcaag 720
gctcgtgaag tcttgatag cgtcattggc aggtatatcg cgctgaagcg cggcgaaatg 780
agaagccgag gaatttcgat tgattgtgaa aatgaagatg gtgtggatct gctcacgtct 840
tacatgactg tgggagacga tgggtactcaa acccatgatt tgaaatgtga tgacaagtct 900
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gaaccgacaa tgaaagtgat gttctcattg tacgccatgg gacggatgga atccgtttgg 1260
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gatgtggctt tcgctcaggt gaaggcagtg gccgccacct taatccataa ctaccaagtt 1440
cacgtggcag acggccaccg cgtgctgccc aattgttcca tcacctcta catgaggaat 1500
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<210> 56

<211> 515

<212> PRT

<213> Sesamum indicum

<220>

<223> SiP288

<400> 56

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Met Val Gly Ile Val Tyr Ile Glu Leu Phe Leu Ser Val Met Trp Phe
  1               5               10               15

```

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Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp
      20               25               30

```

```

Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile
    35               40               45

```

```

His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe
    50               55               60

```

```

His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Met Gly Thr Ala
    65               70               75               80

```

```

Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe
    85               90               95

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```

Pro Lys Gly Pro Lys Phe Arg Glu Ile Phe Asp Val Leu Gly Asp Gly
   100               105               110

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Ile Phe Asn Ala Asp Ser Glu Ser Trp Arg Asp Gln Arg Arg Val Ala

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115	120	125
Arg Ala Leu Ile Ser His His Gly Phe Leu Arg Phe Leu Ala Lys Ile 130 135 140		
Ser Arg Glu Lys Val Glu Lys Gly Leu Ile Pro Val Leu Glu Thr Val 145 150 155 160		
Cys Leu Glu Asn Arg Val Val Asp Leu Gln Asp Leu Phe Gln Arg Leu 165 170 175		
Thr Phe Asp Thr Thr Cys Thr Phe Val Thr Gly Tyr Asp Pro Gly Cys 180 185 190		
Leu Ser Val Asp Leu Pro Asp Val Pro Phe Ser Lys Ala Leu Asp Asp 195 200 205		
Ala Glu Glu Ala Ile Phe Met Arg His Val Val Pro Glu Lys Ile Trp 210 215 220		
Lys Leu Gln Arg Trp Phe Gly Val Gly Ser Glu Arg Lys Leu Ser Lys 225 230 235 240		
Ala Arg Glu Val Leu Asp Ser Val Ile Gly Arg Tyr Ile Ala Leu Lys 245 250 255		
Arg Gly Glu Met Arg Ser Arg Gly Ile Ser Ile Asp Cys Glu Asn Glu 260 265 270		
Asp Gly Val Asp Leu Leu Thr Ser Tyr Met Thr Val Gly Asp Asp Gly 275 280 285		
Thr Gln Thr His Asp Leu Lys Cys Asp Asp Lys Phe Leu Arg Asp Thr 290 295 300		
Ile Leu Asn Leu Met Ile Ala Gly Arg Asp Thr Thr Ser Ser Ala Leu 305 310 315 320		
Thr Trp Phe Ile Trp Leu Val Ser Thr His Ala Glu Val Glu Lys Arg 325 330 335		
Ile Arg Asp Glu Leu Lys Ser Phe Leu Pro Ala Gly Glu Arg Glu Lys 340 345 350		
Trp Arg Val Phe Gly Val Glu Glu Thr Lys Lys Leu Val Tyr Met His 355 360 365		
Gly Ala Ile Cys Glu Ala Leu Arg Leu Tyr Pro Pro Val Pro Phe Gln 370 375 380		
His Lys Glu Pro Val Glu Pro Asp Ile Leu Pro Ser Gly His Phe Val 385 390 395 400		
Glu Pro Thr Met Lys Val Met Phe Ser Leu Tyr Ala Met Gly Arg Met 405 410 415		
Glu Ser Val Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp		

420	425	430
Ile Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu		
435	440	445
Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe		
450	455	460
Ala Gln Val Lys Ala Val Ala Ala Thr Leu Ile His Asn Tyr Gln Val		
465	470	475
His Val Ala Asp Gly His Arg Val Leu Pro Asn Cys Ser Ile Ile Leu		
485	490	495
Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala		
500	505	510

Lys Lys Asn  
515

<210> 57  
<211> 1494  
<212> DNA  
<213> Sesamum indicum

<220>  
<223> SiP168

<400> 57

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gccaaactct	ccaaaaccta	cgggcccctg	atgcgtctca	agctgggaac	catgacaaca	240
gttggttgat	cctccccgga	aatctccagg	atcgtgctgc	aacaatatga	ccaagttttc	300
tccagccgaa	cacacgcaga	tgccatccga	gcacttgacc	accacaaaca	ttccgtcgcc	360
tggataccgg	cggacaatca	gtggcggaaa	atccgtaaac	tgtgcaaaga	gaagatgttt	420
tggggccaaa	agcttgatgc	gaaccagggc	ctgaggaggg	agaagttgcg	taatttgcaa	480
gactatgtga	atgaatgctg	cgttagtggc	caggctcgtg	atattggtgt	agctgccttt	540
acgacgaccc	ttaatctgat	atcggccact	cttttctcgg	tggattttgc	tgatttttgt	600
tctggttcgt	ctcaagagct	taaggatgtt	atgagcggga	tagcgtctat	catcggccga	660
ccaaattttg	ctgattgttt	ccctcttctt	cggctgggtg	atccacaggg	catcttccgc	720
cagaccacgt	tacatttcaa	caagtgtttt	aagatctttg	atgaaattat	ccgtcaaagg	780
ctacagacca	atgattcggg	gacgaaaagt	gacatgctga	aagagcttct	tgaaatcaac	840
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gtcgcaggaa	cggacacaac	ttcagttaca	gtggaatggg	caatgacgga	gctagtgcgc	960
cacctgaga	aaatgtcgaa	agccagaaat	gagttaagaa	atgtggtggg	actgaataaa	1020
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atcaatggct	atatagtccc	taaaggagca	caagttctca	tgaacgtgtg	ggccatcggc	1200
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tgcgtggggc	tgccgttagc	ctatcgtatg	atccatctcg	tgcttgccac	tttcataagc	1380
gactatgatt	ggaaacttga	aggagggctg	aaaactgaag	aaatggacat	gagtgaaaag	1440
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<210> 58  
<211> 498  
<212> PRT  
<213> Sesamum indicum

<220>  
<223> SiP168

<400> 58

Met	Asp	Leu	Leu	Leu	Ser	Leu	Val	Leu	Leu	Leu	Cys	Ser	Ala	Ala	Cys
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Ile	Trp	Phe	Leu	Arg	Val	Val	Leu	Lys	Pro	Asn	Pro	Gly	Pro	Arg	Lys
			20					25					30		
Ser	Ala	Asn	Leu	Pro	Pro	Gly	Pro	Lys	Pro	Leu	Pro	Ile	Ile	Gly	Asn
		35					40					45			
Ile	Leu	Glu	Leu	Gly	Glu	Lys	Pro	His	Gln	Ser	Leu	Ala	Lys	Leu	Ser
	50					55					60				
Lys	Thr	Tyr	Gly	Pro	Leu	Met	Arg	Leu	Lys	Leu	Gly	Thr	Met	Thr	Thr
65					70					75					80
Val	Val	Val	Ser	Ser	Pro	Glu	Ile	Ser	Arg	Ile	Val	Leu	Gln	Gln	Tyr
				85					90					95	
Asp	Gln	Val	Phe	Ser	Ser	Arg	Thr	His	Ala	Asp	Ala	Ile	Arg	Ala	Leu
		100						105					110		
Asp	His	His	Lys	His	Ser	Val	Ala	Trp	Ile	Pro	Ala	Asp	Asn	Gln	Trp
		115					120					125			
Arg	Lys	Ile	Arg	Lys	Leu	Cys	Lys	Glu	Lys	Met	Phe	Ser	Gly	Gln	Lys
	130					135					140				
Leu	Asp	Ala	Asn	Gln	Gly	Leu	Arg	Arg	Glu	Lys	Leu	Arg	Asn	Leu	Gln
145					150					155					160
Asp	Tyr	Val	Asn	Glu	Cys	Cys	Val	Ser	Gly	Gln	Val	Val	Asp	Ile	Gly
				165					170					175	
Val	Ala	Ala	Phe	Thr	Thr	Thr	Leu	Asn	Leu	Ile	Ser	Ala	Thr	Leu	Phe
			180					185					190		
Ser	Val	Asp	Phe	Ala	Asp	Phe	Gly	Ser	Gly	Ser	Ser	Gln	Glu	Leu	Lys
		195					200					205			
Asp	Val	Met	Ser	Gly	Ile	Ala	Ser	Ile	Ile	Gly	Arg	Pro	Asn	Phe	Ala
	210					215					220				
Asp	Cys	Phe	Pro	Leu	Leu	Arg	Leu	Val	Asp	Pro	Gln	Gly	Ile	Phe	Arg
225					230				235						240
Gln	Thr	Thr	Leu	His	Phe	Asn	Lys	Cys	Phe	Lys	Ile	Phe	Asp	Glu	Ile
				245					250					255	

Ile Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met  
 260 265 270  
 Leu Lys Glu Leu Leu Glu Ile Asn Gln Lys Asp Glu Ser Glu Leu Ser  
 275 280 285  
 Phe Asp Glu Ile Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr  
 290 295 300  
 Asp Thr Thr Ser Val Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg  
 305 310 315 320  
 His Pro Glu Lys Met Ser Lys Ala Arg Asn Glu Leu Arg Asn Val Val  
 325 330 335  
 Gly Leu Asn Lys Glu Ile Gln Glu Ser Asp Ile Ser Arg Leu Pro Tyr  
 340 345 350  
 Leu Arg Ala Val Val Lys Glu Ser Phe Arg Leu His Pro Ala Thr Pro  
 355 360 365  
 Leu Ser Val Pro His Lys Ala Asp Glu Glu Ala Glu Ile Asn Gly Tyr  
 370 375 380  
 Ile Val Pro Lys Gly Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly  
 385 390 395 400  
 Arg Asp Ser Ser Ile Trp Arg Asn Pro Asp Val Phe Met Pro Glu Arg  
 405 410 415  
 Phe Leu Glu Thr Glu Ile Asp Val Arg Gly Gln His Phe Glu Leu Leu  
 420 425 430  
 Pro Phe Gly Gly Gly Arg Arg Ile Cys Val Gly Leu Pro Leu Ala Tyr  
 435 440 445  
 Arg Met Ile His Leu Val Leu Ala Thr Phe Ile Ser Asp Tyr Asp Trp  
 450 455 460  
 Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys  
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 Phe Gly Leu Thr Leu Gln Lys Ala Ile Pro Leu Lys Ala Leu Pro Val  
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 Lys Ile

<210> 59  
 <211> 1545  
 <212> DNA  
 <213> Sesamum indicum

<220>  
 <223> SiP236

<400> 59  
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ggtctcattg tccgcccctt tcacagaatg gacgagaaaa ctgca 1545

<210> 60  
<211> 515  
<212> PRT  
<213> Sesamum indicum

<220>  
<223> SiP236

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20 25 30  
Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr  
35 40 45  
Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala  
50 55 60  
Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg  
65 70 75 80  
Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys  
85 90 95  
Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu

100					105					110						
Gly	Asp	Leu	Phe	Gly	Glu	Gly	Ile	Phe	Ala	Ile	Asp	Gly	His	Lys	Trp	
115					120					125						
Arg	Glu	Gln	Arg	Lys	Val	Ser	Ser	Leu	Glu	Phe	Ser	Thr	Arg	Val	Leu	
130					135					140						
Arg	Asp	Tyr	Ser	Ser	Ile	Val	Phe	Arg	Lys	Asn	Ala	Val	Arg	Leu	Ala	
145					150					155					160	
Lys	Ile	Leu	Ser	Gly	Ala	Ala	Thr	Ser	Asn	Gln	Pro	Val	Asp	Ile	Gln	
165					170					175						
Asp	Leu	Phe	Met	Lys	Ser	Thr	Phe	Asp	Ser	Ile	Ser	Glu	Val	Ala	Leu	
180					185					190						
Gly	Val	Glu	Leu	Asp	Ser	Leu	Gly	Gly	Ser	Asn	Glu	Glu	Gly	Ala	Lys	
195					200					205						
Phe	Ser	Ile	Ala	Ala	Asp	Asp	Val	Ser	Met	Arg	Thr	Leu	Trp	Arg	Tyr	
210					215					220						
Val	Asp	Val	Leu	Trp	Lys	Leu	Lys	Arg	Ala	Leu	Asn	Val	Gly	Ser	Glu	
225					230					235					240	
Ala	Lys	Leu	Lys	Lys	Ser	Leu	Gln	Val	Val	Asp	Glu	Phe	Val	Tyr	Lys	
245					250					255						
Leu	Ile	His	Ser	Arg	Thr	Gln	Gln	Met	Asn	Met	Pro	Gly	Asn	Asp	Ser	
260					265					270						
Val	Met	Gln	Leu	Lys	Lys	Asp	Asp	Ile	Leu	Ser	Arg	Phe	Leu	Gln	Leu	
275					280					285						
Thr	Glu	Ala	Thr	Pro	Lys	Tyr	Leu	Arg	Asp	Ile	Thr	Ile	Ser	Phe	Ile	
290					295					300						
Val	Ala	Gly	Lys	Asp	Thr	Thr	Ala	Thr	Thr	Leu	Ser	Trp	Phe	Ile	Tyr	
305					310					315					320	
Met	Leu	Cys	Lys	Tyr	Pro	His	Val	Gln	Glu	Lys	Val	Glu	Gln	Glu	Ile	
325					330					335						
Lys	Asp	Ala	Thr	Gly	Cys	Lys	Glu	Val	Ala	Asp	Ile	Ser	Glu	Phe	Ser	
340					345					350						
Ala	Cys	Val	Thr	Glu	Glu	Ala	Leu	Gly	Lys	Met	His	Tyr	Leu	His	Ala	
355					360					365						
Ala	Leu	Thr	Glu	Thr	Leu	Arg	Ile	Tyr	Pro	Ala	Val	Ala	Val	Asp	Ala	
370					375					380						
Lys	Gln	Cys	Leu	Cys	Asp	Asp	Ile	Met	Pro	Asp	Gly	Phe	Ser	Val	Lys	
385					390					395					400	
Lys	Gly	Asp	Met	Val	Ala	Tyr	Gln	Pro	Tyr	Ala	Met	Gly	Arg	Met	Lys	

405	410	415
Ser Ile Trp Gly Asn Asp Ala Glu Glu Phe Lys Pro Glu Arg Trp Leu		
420	425	430
Asp Lys Asn Gly Cys Phe Gln Gln Ala Ser Pro Phe Lys Phe Thr Ala		
435	440	445
Phe Gln Ala Gly Pro Arg Leu Cys Leu Gly Lys Glu Phe Ala Tyr Arg		
450	455	460
Gln Met Lys Ile Phe Ser Ala Ile Leu Leu Arg Phe Phe Thr Met Lys		
465	470	475
Leu Ser Asp Glu Arg Lys Thr Val Asn Tyr Arg Pro Met Leu Thr Leu		
485	490	495
Leu Ile Asp Gly Gly Leu Ile Val Arg Pro Phe His Arg Met Asp Glu		
500	505	510
Lys Thr Ala		
515		

<210> 61  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, Bam-SST-FW2

<400> 61  
 tggatcccaa ctcatagagt actcaaaaac gctt

34

<210> 62  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, SiP189-Nco-RV

<400> 62  
 gcaaatgata aaccatggtg ttct

24

<210> 63  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, GR-SST-RV1

<400> 63

cacatgaacg agacgaactg gggtttgg

27

<210> 64

<211> 506

<212> PRT

<213> Sesamum radiatum

<220>

<223> SrSiP189

<400> 64

Met	Glu	Ala	Glu	Met	Leu	Tyr	Ser	Ala	Leu	Ala	Leu	Thr	Phe	Ala	Ile
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Phe	Met	Val	Tyr	Arg	Ile	Leu	Ser	Asn	Ser	Gln	Glu	Lys	Ser	Ser	Leu
			20					25					30		
Ile	Lys	Leu	Pro	Pro	Ser	Pro	Pro	Gly	Trp	Leu	Pro	Val	Ile	Gly	His
		35					40					45			
Val	His	Leu	Met	Lys	Asn	Leu	Leu	His	Arg	Thr	Leu	Tyr	Asp	Phe	Ser
	50					55					60				
Gln	Lys	Leu	Gly	Pro	Ile	Phe	Ser	Leu	Arg	Phe	Gly	Thr	Arg	Leu	Val
65					70					75					80
Val	Val	Val	Ser	Ser	Ser	Ser	Leu	Val	Glu	Glu	Cys	Phe	Thr	Lys	Tyr
			85						90					95	
Asp	Ile	Val	Leu	Ala	Asn	Arg	Pro	Gln	Pro	Ser	Val	Asp	Arg	Arg	Ser
		100						105					110		
Leu	Gly	Phe	Ser	Thr	Thr	Ser	Val	Ile	Gly	Ala	Pro	Tyr	Gly	Asp	His
		115					120					125			
Trp	Arg	Asn	Leu	Arg	Lys	Leu	Cys	Asp	Leu	Glu	Val	Phe	Ala	Pro	Thr
	130					135					140				
Arg	Leu	Ala	Ser	Phe	Leu	Ser	Ile	Arg	Leu	Asp	Glu	Arg	Asp	Arg	Met
145					150					155					160
Ile	Ser	Ser	Leu	Tyr	Lys	Ile	Ser	Ser	Ala	Gly	Phe	Ala	Lys	Val	Asn
			165						170					175	
Leu	Glu	Thr	Lys	Ile	Val	Glu	Leu	Thr	Phe	Asn	Asn	Ile	Met	Arg	Met
		180						185					190		
Val	Ala	Gly	Lys	Arg	Tyr	Tyr	Gly	Glu	Glu	Ala	Glu	Asp	Asp	Glu	Glu
		195					200					205			

Ala	Lys	Arg	Phe	Arg	Asp	Leu	Thr	Lys	Glu	Ala	Leu	Glu	Leu	Thr	Ser	210	215	220	
Ala	Ser	Asn	Pro	Gly	Glu	Ile	Phe	Pro	Ile	Leu	Arg	Trp	Leu	Gly	Phe	225	230	235	240
Asn	Gly	Leu	Glu	Lys	Lys	Leu	Ala	Val	His	Ala	Arg	Lys	Thr	Asp	Glu	245	250	255	
Phe	Met	Gln	Gly	Leu	Leu	Asp	Glu	His	Arg	Arg	Gly	Glu	Arg	Gln	Asn	260	265	270	
Thr	Met	Val	Asp	His	Leu	Leu	Ser	Leu	Gln	Glu	Ser	Gln	Pro	Glu	Tyr	275	280	285	
Tyr	Thr	Asp	Glu	Ile	Ile	Thr	Gly	Leu	Ile	Val	Ala	Leu	Ile	Ile	Ala	290	295	300	
Gly	Thr	Asp	Ala	Ser	Val	Val	Thr	Thr	Glu	Trp	Ala	Met	Ser	Leu	Ile	305	310	315	320
Leu	Asn	His	Pro	Gln	Val	Leu	Glu	Lys	Ala	Arg	Lys	Glu	Leu	Asp	Thr	325	330	335	
Leu	Val	Gly	His	Glu	Arg	Met	Val	Asp	Glu	His	Asp	Leu	Pro	Lys	Leu	340	345	350	
Arg	Tyr	Leu	His	Cys	Ile	Val	Leu	Glu	Thr	Leu	Arg	Leu	Phe	Pro	Ser	355	360	365	
Val	Pro	Thr	Leu	Val	Pro	His	Glu	Pro	Ser	Glu	Asp	Cys	Lys	Ile	Gly	370	375	380	
Gly	Tyr	Asn	Val	Pro	Lys	Gly	Thr	Met	Ile	Leu	Val	Asn	Ala	Trp	Ala	385	390	395	400
Ile	His	Arg	Asp	Pro	Lys	Val	Trp	Asp	Asp	Pro	Leu	Ser	Phe	Lys	Pro	405	410	415	
Asp	Arg	Phe	Glu	Thr	Met	Glu	Val	Glu	Thr	His	Lys	Leu	Leu	Pro	Phe	420	425	430	
Gly	Met	Gly	Arg	Arg	Ala	Cys	Pro	Gly	Ala	Gly	Leu	Ala	Gln	Lys	Phe	435	440	445	
Val	Gly	Leu	Ala	Leu	Gly	Ser	Leu	Ile	Gln	Cys	Phe	Glu	Trp	Glu	Arg	450	455	460	
Met	Ser	Ala	Glu	Lys	Ile	Asp	Leu	Asn	Glu	Gly	Ser	Gly	Ile	Thr	Leu	465	470	475	480
Pro	Lys	Ala	Lys	Thr	Leu	Glu	Ala	Met	Cys	Lys	Pro	Arg	His	Ile	Met	485	490	495	
Glu	Arg	Val	Leu	Arg	Gln	Val	Ser	Asn	Val							500	505		

<210> 65  
 <211> 1518  
 <212> DNA  
 <213> *Sesamum radiatum*

<220>  
 <223> SrSiP189

<400> 65  
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 agaattcttt ctaattcgca ggagaaaagc agcctgatta agctgccgcc gagcccgcgc 120  
 gggttggtcc cggatgatcg ccacgttcat ctcatgaaaa atctcctcca tagaacacta 180  
 tacgacttct cccagaaact gggaccata tttccctcc gggtcggcac ccgcctcgtg 240  
 gtagtgggtg cctcctcctc cctggctcag gaatgtttca ccaagtacga cattgtcttg 300  
 gccaacgcgc ctcagccctc tgcgacccgc cgctcactcg gggtcagcac caccagcgta 360  
 atcggcgccc cgtacgggga ccattggcgc aacctgcgaa agttgtgcga tcttgaagta 420  
 ttgcctccga cccgtctcgc ctggttttta tccatcaggc ttgacgagag ggaccgcatg 480  
 atttcgtcgt tgtacaaaat ctgctcgcgc gggttcgcga aggtgaattt ggagacgaag 540  
 attgttgagc tgacgtttta taacataatg aggatggtgg cggggaagag atactatggg 600  
 gaggaggcgc aggacgacga ggaggcgaag aggttcaggg acctgacgaa ggaggctttg 660  
 gagttgacga gcgcttccaa tcctgggtgag atatttccaa tattgcggtg gcttggtttc 720  
 aatgggttgga agaagaagct ggctgttcac gcgcggaaga cggatgagtt catgcaaggg 780  
 ctgctggacg aacaccgacg gggcgagcgc cagaacacca tggttgatca tttgctttcg 840  
 ttgcaggaat ctcaacctga gtactacact gatgaaatca tcaactggcct catagtgtga 900  
 ttgataattg cgggaacgga tgcacgggtt gtaactacag aatgggcatg gtcccttata 960  
 ctaaactcgc cccaagtact tgaagggtt agaaaagaac tggacactct agtaggacac 1020  
 gaacgcctgg tcgatgaaca tgatctgccc aaactacgtt accttactg catagtcttg 1080  
 gagaccttaa gggtatttcc ttctgttcca acgttggtgc cacacgaacc atcggaggat 1140  
 tgtaaaattg ggggatacaa tgtccccaag gggacaatga tactggtgaa tgcttgggca 1200  
 atacaccgag accccaaggt gtgggacgac cccttgagct ttaagcccga caggtttgag 1260  
 acaatggaag tggagacaca caagctgttg ccgttcggga tgggcaggag agcgtgtccc 1320  
 ggagctggat tggcgagaaa gtttgtgggg ttggctttgg ggctcgctgat tcagtgtttc 1380  
 gagtgggaga gaatgagtg gcgagaaaatt gacttgaacg aagggtcttg gataaccttg 1440  
 cctaaagcta agacgttgga agccatgtgc aaacctagac atatcatgga gagagtctct 1500  
 cgtcagggtt cgaacgct 1518

<210> 66  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, NtUBQ-FW

<400> 66  
 ggaatgcaga tcttcgtcaa

20

<210> 67  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, NtUBQ-RW

<400> 67  
 cctagaaacc accacgga 18

<210> 68  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, SiP189-bam-FW

<400> 68  
 ttttcagcca acatggaagc tgaa 24

<210> 69  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, SiP189-nco-RV

<400> 69  
 gcaaagatc aaccatggtg ttct 24

<210> 70  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, STAR-LF1

<400> 70  
 acgaagttat gcggccaatt aaccc 25

<210> 71  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, STAR-LR1

<400> 71  
ccacctgacg tcgcggccta atacg 25

<210> 72  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, M13-47(F)

<400> 72  
cgccagggtt ttcccagtcg cgac 24

<210> 73  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, RV-M(R)

<400> 73  
gagcggataa caatttcaca cagg 24

<210> 74  
<211> 3069  
<212> DNA  
<213> Sesamun indium

<400> 74  
tacgtggttg taaattaagg tggcatagtc aaagctgtgt aggatggagg aattagacac 60  
ttccccagtc cccacagac tattcccgag ctgaccaa acagtcgaaa gtgtggggcc 120  
caatgaaatt gacagatgac gtctagtgtg gtgtgaatgt gtgatatttt tgcagaatat 180  
tgtaaaagag ggttcaccaa atctcactag tttgtgacta attgactatt tttgcagaaa 240  
attcgtatatt agtatagggt cttgggtcaaa ttaattaatt atataacaaa tgtgatatat 300  
ttaatttggtt attaatTTTT ttatatTTgt tgtgtaatta gttaggattt tatataagaa 360  
tttgaaaaaa tgagatgttt ttttgtaaat caaattacac aatatcatgt attgggtttt 420  
tcgtcctgaa gtcgcttgaa aattgattag atcggcggac ttgaacagac gagtgaatgg 480  
acatgattta aaattttaag gataaatata tatagtatca gttatcaaaa taaaaaattt 540  
ccttcaaaat catggtcttg ttttaagatag ttttttgagt aatgtggcac cataattccc 600  
aagcactaga agtgcaattg taaatccaac ggtacctagt ttaattgata aaattaaagt 660  
ccaaaaattt tcctgagaaa ccaattcgag caaggggtaca tcaaagggtgc caccaggagg 720  
ttaagcaaga aatgtccctt aaactttagg catgagggtat ccctataaaa taaattgacc 780  
taaaaagatt caaatggctt agagtcgaga aaaagactaa gtagaccatt aggggaagccc 840  
acatgcctaa gatcctccag ccgaagtaga ggcctatgag gcagtcagcc tagtgacttg 900  
ggattcccta gctctgaaag aattaatatt gtcccaagaa tctaaggcta catagtagaa 960  
atgaaaacaa agcgaattta aatttgaagc cagcatgatt gaattttttt tttttttttc 1020  
agggtgttta gcaactcaaac atgtacaata aataaacgtg tggctaattt aaagaacatt 1080  
gaaagctggc caagaattat accttttaaa gcgagtggag tttccgatgt ttgagctctc 1140  
attcaatccg ttcacatcta gatgaacaaa cgtctctttt aatggatatcc acgatacctt 1200  
tgtcgagggg atttctcgtc tccttgctag aggattcaat attaccaagg ggtcaaaact 1260

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ctgttaaagt	tttgtgcatg	tcctctatat	gccaaatatt	tggtggttaag	cacgacaaag	1500
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cataggccaa	cccattagct	tgtagggtcac	atattccaac	ataatgtaga	ggctcaagca	1620
caagcagacc	catgccatat	ggcgtccatg	gggtagtcca	ggtgatattg	acgtaagtct	1680
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ggatatcccc	taagctattt	caaaaaatct	aggaacctta	tctgtagcag	actttgttaa	1860
tttttcaa	caagggactc	caacagccaa	gcgataaccc	tcaccaaatt	tgtgaaggat	1920
tcgatattat	ccaaccagtt	gatgatttgc	ttataaagtg	caatcttccc	ccaacaaaaa	1980
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tataaatttc	aatctcttaa	gtgtacacaa	aatacaagat	atttcactct	tttgtatttt	2100
tctaattccc	ataattttat	ctttattttg	tatttttgatt	gaacccgagc	acatctttga	2160
cttgcatcaa	caatattagc	tctaaattaa	acatagaatt	taatgttaaa	atgagaaaag	2220
gaactcatac	agatcggact	caaaacctta	acaccttaata	aagtatgcat	cctaataaaa	2280
agttattacc	aaagtgaat	tatgcttaat	gaaaatcgaa	atcagaagta	gttcttaatt	2340
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tactcttaaa	ttataatcta	attcaatata	cacaacaacc	tatcacatta	atatacaata	2460
tgaaaggtca	ataaaatatt	tacgctggca	aacctcccca	gtagaattcg	ggcacatatg	2520
aagtgttaac	cattcaaata	tggacaaagg	aacactagag	acacgaagtt	tatttcaaag	2580
gaaaattttg	tctaaaattg	aatttaatta	aatttaaatt	aattatataa	taaatataat	2640
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ttaattaata	aataactttt	acaagacca	ggccaccaac	tcccgtccac	atgaaagaat	2760
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aatcaaat	ttaattttta	ctttatccaa	ggcaagaaaa	caaaaaatgc	ataaattcac	2880
gttctaattc	atcaatactc	aagaaatagc	atacttgatt	tgaactgaga	tttgtcactt	2940
tcctacaaat	tctgcagact	atgaaaacga	catcaaccaa	ccaatatcca	ctctctatat	3000
aatagcatc	acttcactag	caattttctca	tcaactcata	gagtactcaa	aaacgctttt	3060
tcagccaac						3069

<210> 75

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, gSST-FW1

<400> 75

aatgaaattg acagatgacg tctagtgtgta

29

<210> 76

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, gSST-RV2

<400> 76

ctgcgaatta gaaagaattc tgtaaaccat

30

<210> 77  
 <211> 2815  
 <212> DNA  
 <213> *Sesamum radiatum*

<400> 77  
 tagtgtagtg tgaatgtgtg atatTTTTgc agtatatata ttgtaaaaga ggattaacca 60  
 aatctctcta gtTCgtgatt atgactatTT ttgcagaaaa tttgtattta gtttaggggt 120  
 ggtaaaatct aatttataga gtaaatatga tgtatttatt ttgtgattga ttacttttat 180  
 atttattgta taattagtta taatttgata aagtgtgata ttttttataa attagattac 240  
 atattattat gtactgagtt tttcgttctg atgccattta aaaattgggt aggtcggcga 300  
 cttgaactga cgagtgaagg gacttgattt aacattttta ggatatatat atatatgtacc 360  
 agttatcaaa ataaaagttt tctttcaaaa tcatagtttt gtttaagata attttgtgag 420  
 tatatgttgc accacaattc ccaagcacta taagtgcac tgtaggtcta attggaccta 480  
 gtttagttga caaaattgaa gtccaagaat atcttcaaga agccaattcg tgtaatggta 540  
 cgtcaaaggt gccaccaggg aatcaagtag gaaatttccc ctaaatgtta ggcatgaggt 600  
 gccactataa agaaaattga cccaaagaga tacaagtatc ttagagtcga gaagaagact 660  
 acgtagacca ttaggggaagt ccacatgcct aagattctgc agctgaagca caggcctagg 720  
 tacggtcagc ccagggactc gagatccctc agctctcaaa gaattgggtat tggcccagga 780  
 atctaaggct acatagcaaa aacgaaaata aaacaaactt aaatttgaag tcaacgggat 840  
 tgaatcctat tttctcgggt gttcaaactc aagcatgtaa aataaataaa cgtgtgacta 900  
 atttacaana cactgaaaac taattacaaa ttatacctta aaagcatgtg tagtttttaa 960  
 cgtttgagct ttcgtcaatc cattcacgta gagataaacg gacgtctcct ctaagggtat 1020  
 ccacaatacc attggcgagg agatttcttg tctattagag gattcgagat taccatggag 1080  
 ttagaactat aaacctaaag aagatcgaga aaatactatt agattagtgt tctcaatctc 1140  
 aattctcaag ctttcaaacc tagttaaaag cttgagaaaa tttgtgcgta gatatgtttt 1200  
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 gtggtggtta gcacaacaaa gttatgtgaa aagaaattgt attagcacta cgttgaataa 1380  
 gattgtcttc tactaataga tgatagaggg caacctatgg cttgtcgggt acttattcca 1440  
 acataatgta gaggcccaag catgataaga cctatgccac aggacgtcct tgggtgggtc 1500  
 aagtgatatt gacgtaagac cttttaacct acttcggcag gctttagcca taacctccag 1560  
 cctgtgaaac ccgatcagat gaggatatcc cctcagcccc tccaaaaatc taggaatctc 1620  
 atccgcagca gatttcggta tcttttctca gaagatcaaa aaactctaac cactaagaga 1680  
 taaccccccc cacaaaatta atggaaaatt tggccttatc taactggcta ataggttgcc 1740  
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 aacaagatat ttactcatt tgttttctct tagttcctat aattttatct ttcttgcac 1920  
 aacaatattt gctctaaatt aaatatagaa tttaattgta aaatgagaaa acggactcaa 1980  
 aaccagaaca cctaataaag tatgcatctt aataaaaagt tattacgaag gagaaaaata 2040  
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 atattgcaag tcatcctcac tttctcatcc atagacagtc acacctacc cecatatttc 2160  
 atacttttaa attattatct aatttaatat acgcatacant tcataatata taatacgaaa 2220  
 ggtaataaaa atatttacgc tagcaaactt cttcagtaga attcatgtac ataagaagtg 2280  
 ttgaccattc aaatatggaa aaagaaacac tagagataag aaacttagtt gtgaagcaga 2340  
 aaatatttaa gttggttgggt tggatttgaa ctaatttaata taataaatat aatatatcgt 2400  
 gtaaatgtaa aaacgactat taacatcaat taataaataa ttttctgtta gtgaagatgg 2460  
 actacaagac ctaggccacc aacccccatc cactgaatg aatgggtaac cgctaagtcc 2520  
 atatttcagt actccggcgt ctgcaaaaaac gctttttcca caaaaatcaa attttaagtt 2580  
 ttacttttat ctaggcaag aaaacaaaaat atgcatagat tcacgttcaa attcatcaat 2640  
 gctcaagaaa tagcatactt gatttgaact gagatttgtc actatcctac aaattctgca 2700  
 cactatgaaa acgacatcaa ccaacaaaaa tccactctct ataaatacca tcaattcact 2760  
 agcaatttct catcaactca taacgtactc aaataaacac gctttttcag ccaac 2815

<210> 78  
<211> 507  
<212> PRT  
<213> Sesumum alatum

<400> 78

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Ile	Met	Val	His	Arg	Ile	Leu	Ser	Asn	Ser	Gln	Asn	Lys	Arg	Ser	Leu
			20					25					30		
Ile	Asn	Leu	Pro	Pro	Ser	Pro	Pro	Gly	Trp	Leu	Pro	Ile	Ile	Gly	His
		35						40				45			
Leu	His	Leu	Ile	Lys	Asn	Pro	Leu	His	Arg	Thr	Leu	Tyr	Asp	Cys	Ser
	50					55					60				
Gln	Lys	Leu	Gly	Ser	Ile	Phe	Ser	Val	Trp	Phe	Gly	Ser	Arg	Leu	Val
65					70					75					80
Val	Val	Val	Ser	Ser	Ser	Ser	Leu	Val	Glu	Glu	Cys	Phe	Thr	Lys	Tyr
				85					90					95	
Asp	Ile	Val	Leu	Ala	Asn	Arg	Pro	Asp	Leu	His	Leu	Asp	Leu	Arg	Ser
		100						105					110		
Leu	Gly	Ala	Ser	Thr	Ile	Ser	Val	Ile	Gly	Ala	Pro	Tyr	Gly	Asp	His
	115						120					125			
Trp	Arg	Asn	Leu	Arg	Lys	Leu	Cys	Asp	Leu	Glu	Val	Phe	Ala	Pro	Thr
	130					135					140				
Arg	Leu	Ala	Ser	Phe	Leu	Ser	Ile	Arg	Arg	Asp	Glu	Arg	Asp	Arg	Met
145					150					155					160
Ile	Ser	Gly	Leu	Tyr	Lys	Ile	Ser	Ser	Ala	Gly	Leu	Ala	Lys	Val	Asn
			165						170					175	
Leu	Glu	Ala	Lys	Ile	Ala	Glu	Leu	Thr	Phe	Asn	Asn	Leu	Met	Arg	Met
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Leu	Ala	Gly	Lys	Ile	Tyr	Tyr	Gly	Glu	Glu	Ala	Glu	Asp	Glu	Glu	Glu
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and use thereof

<130> SU0411

<150> JP 2003-341313  
<151> 2003-09-30

<150> JP 2003-432383  
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50 55 60  
Gln Lys Leu Gly Pro Ile Phe Ser Ile Arg Phe Gly Ser Arg Leu Val  
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Asp Ile Val Leu Ala Asn Arg Pro Gln Ala Ser Val Asp Arg Arg Ser  
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Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His  
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Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr  
130 135 140  
Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met  
145 150 155 160

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Ile Ser Ala Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn  
 165 170 175  
 Leu Glu Ala Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met  
 180 185 190  
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 195 200 205  
 Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser  
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 Ala Ser Asn Pro Gly Glu Ile Phe Pro Ile Leu Arg Trp Leu Gly Cys  
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 Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn  
 260 265 270  
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 Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala  
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<210> 6  
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<210> 12  
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<210> 24

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<212> DNA

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

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ggatgttctg tggaagttaa a

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&lt;211&gt; 21

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

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&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
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&lt;210&gt; 38

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Synthesized Primer Sequence, SiP236-BamHI-FW

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ggatccttca cttcacttca ttgctcaatg gcaaa 35

<210> 52  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, SiP236-XhoI-RV

<400> 52  
 ctcgagaaca gctgagaccc cacagcaatc taa

33

<210> 53  
 <211> 1503  
 <212> DNA  
 <213> Sesamum indicum

<220>  
 <223> SiP249

<400> 53  
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 cccttcctcg ggaacttgct ccaatacaac ccctccgac tccatctccg cctgacaaaa 180  
 ctctcagaaa agtacggccc gcttatgtac atgacgttcg tcgaaagcc cgtgggttg 240  
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 tcgagcagga tgatatctag gtttgactg gggaagaggt acgacgagga gaacggggccg 600  
 gaaaagagga gggtcgacag gattctgcag ctgcttcagt tgggtgcggt ggaaattttc 660  
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 ctgtattgct tccactggga attgccgcct ggaatggtag aagatgacgt tgatatggac 1440  
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 ctg 1503

<210> 54  
 <211> 501  
 <212> PRT  
 <213> Sesamum indicum

<220>

&lt;223&gt; SiP249

&lt;400&gt; 54

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Leu Leu Val Arg Arg Arg Arg Asn Ser Pro Ala Gly Arg Lys Leu Arg  
 20 25 30

Arg Pro Pro Gly Pro Pro Gly Leu Pro Phe Leu Gly Asn Leu Leu Gln  
 35 40 45

Tyr Asn Pro Ser Asp Leu His Leu Arg Leu Thr Lys Leu Ser Glu Lys  
 50 55 60

Tyr Gly Pro Leu Met Tyr Met Thr Phe Val Gly Lys Pro Val Val Val  
 65 70 75 80

Ile Ser Ser Ala Arg Val Ala Lys Glu Ala Leu Lys Tyr Asn Asp Leu  
 85 90 95

Ala Phe Ser Ser Arg Pro Ser Thr Ile Ala Ser Arg Lys Val Ala Tyr  
 100 105 110

Asn Asn Ser Asp Ile Ser Met Ser Pro Tyr Thr Glu Tyr Trp Arg Glu  
 115 120 125

Leu Arg Lys Met Val Val Leu Arg Leu Phe Thr Val Lys Gln Val Asn  
 130 135 140

Ser Phe Arg Pro Ala Arg Glu Glu Glu Val Ala Arg Met Val Lys Glu  
 145 150 155 160

Ile Ser Arg Arg Ala Asn Ala His Gln Pro Val Asn Ile Asn Glu Ile  
 165 170 175

Ala Leu Ser Leu Ser Ser Arg Met Ile Ser Arg Phe Ala Leu Gly Lys  
 180 185 190

Arg Tyr Asp Glu Glu Asn Gly Pro Glu Lys Arg Arg Phe Asp Arg Ile  
 195 200 205

Leu Gln Leu Leu Gln Leu Val Ser Val Glu Ile Phe Phe Gly Asp Tyr  
 210 215 220

Ser Pro Trp Leu Gly Trp Ile Asp Arg Leu Cys Gly Lys Val Ser Gln  
 225 230 235 240

Leu Glu Lys Ala Phe Lys Asp Leu Asp Ser Leu Tyr Glu Glu Met Ile  
 245 250 255

Ala Glu His Leu Ser Pro Asn Arg Pro Glu Ser Met Asn Gly Asp Ile  
 260 265 270

Leu Asp Met Leu Ile Gln Met Lys Glu Asp Arg Ser Ser Thr Val Gln  
 275 280 285

Ile Asp Trp Asp His Ile Lys Gly Val Leu Met Asn Met Phe Val Ala  
 290 295 300  
 Gly Thr Asp Thr Thr Ala Ala Thr Ile Thr Trp Ala Met Thr Ala Leu  
 305 310 315 320  
 Ile Lys Lys Pro Gln Val Leu Asn Lys Val Gln Gln Glu Ile Arg Ser  
 325 330 335  
 Val Val Gly Lys Lys Gly Ser Val Ala Glu Asp Asp Ile Gln Lys Leu  
 340 345 350  
 Pro Tyr Phe Lys Ala Val Val Lys Glu Thr Leu Arg Leu Tyr Ala Pro  
 355 360 365  
 Ala Pro Leu Ser Leu Pro Arg Leu Thr Ile Lys Ser Ser Val Ile Asp  
 370 375 380  
 Gly Tyr Asp Ile Glu Pro Asn Thr Ile Val Tyr Val Asn Val Trp Ala  
 385 390 395 400  
 Ile Ser Arg Asp Lys Asp Phe Trp Glu Asn Pro Asp Glu Phe Leu Pro  
 405 410 415  
 Glu Arg Phe Leu Asn Ser Ser Val Asp Phe Lys Gly Gln Asp Phe Gly  
 420 425 430  
 Phe Leu Pro Phe Gly Ser Gly Arg Arg Val Cys Pro Gly Met Ala Leu  
 435 440 445  
 Gly Thr Ala Glu Val Glu Val Ser Leu Ala Asn Ile Leu Tyr Cys Phe  
 450 455 460  
 His Trp Glu Leu Pro Pro Gly Met Val Glu Asp Asp Val Asp Met Asp  
 465 470 475 480  
 Phe Leu Pro Gly Ile Thr Thr His Lys Lys Asn Ala Leu Tyr Leu Met  
 485 490 495  
 Ala Lys Ser Tyr Leu  
 500

<210> 55  
 <211> 1545  
 <212> DNA  
 <213> Sesamum indicum

<220>  
 <223> SiP288

<400> 55  
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 cttctgcttc acgtgagccg gattcacgac aattgcacgg agattatggg gaagtcccga 180  
 cggggaactt ttcatttccg ggtccctgg ttggctgata tggacatgat ggggactgct 240  
 gatcctgaga atgttacta cattatgagc gcgaacttcc agaatttccc gaaaggcccc 300

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aagttcaggg aaatttttga tgttcttggg gatgggattt tcaatgcaga ttcggagtc 360
tggagggacc agagaagggt tgccagggcc ctgatttctc accatgggtt cctccggtt 420
ctggcgaaga tcagccgtga gaaggtagag aaaggcctga ttccagttct tgaaacggtg 480
tgcctggaag atcgggtggt cgatttgcag gatttgttcc agaggttgac gtttgataca 540
acttgtacat ttgttactgg ttatgatcct ggatgcttgt ctgttgattt gcctgatgtt 600
cctttctcga aagccctaga tgatgccgaa gaagcgatat tcatgcgcca tgtggttcct 660
gaaaagattt ggaaacttca gaggttggtt ggggttggat ctgagagaaa attgagcaag 720
gctcgtgaag tcttggatag cgtcattggc aggtatacgc cgctgaagcg cggcgaagt 780
agaagccgag gaatttcgat tgattgtgaa aatgaagatg gtgtggatct gctcacgtct 840
tacaatgactg tgggagacga tgggtactcaa acccatgatt tgaaatgtga tgacaagttc 900
ttgagggaca cgatactgaa tctaatgatt gcagggcggg acacgacgag ttctgtctctg 960
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gaaccgacaa tgaaagtgat gttctcattg tacgcatagg gacggatgga atccgtttgg 1260
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cacgagccct catacaagtt cttggcttcc aatgctggtc cgaggacttg cttgggggaa 1380
gatgtggctt tcgctcaggt gaaggcagtg gccgccacct taatccataa ctaccaagtt 1440
cacgtggcag acggccaccg cgtgctgccc aattgttcca tcatcctcta catgaggaat 1500
ggattgaagg ttaggttgc caatagatgg tctgctaaga aaat 1545

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&lt;210&gt; 56

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Sesamum indicum

&lt;220&gt;

&lt;223&gt; SiP288

&lt;400&gt; 56

Met Val Gly Ile Val Tyr Ile Glu Leu Phe Leu Ser Val Met Trp Phe

1

Met Ala Leu Trp Val Trp Leu Asn Tyr Arg Ala Leu Ala Trp Asn Trp

20

25

30

Pro Val Ile Gly Met Leu Pro Thr Leu Leu Leu His Val Ser Arg Ile

35

40

45

His Asp Asn Cys Thr Glu Ile Met Gly Lys Ser Arg Arg Gly Thr Phe

50

55

60

His Phe Arg Gly Pro Trp Leu Ala Asp Met Asp Met Met Gly Thr Ala

65

70

75

80

Asp Pro Glu Asn Val His Tyr Ile Met Ser Ala Asn Phe Gln Asn Phe

85

90

95

Pro Lys Gly Pro Lys Phe Arg Glu Ile Phe Asp Val Leu Gly Asp Gly

100

105

110

Ile Phe Asn Ala Asp Ser Glu Ser Trp Arg Asp Gln Arg Arg Val Ala

115

120

125

Arg Ala Leu Ile Ser His His Gly Phe Leu Arg Phe Leu Ala Lys Ile

130 135 140  
 Ser Arg Glu Lys Val Glu Lys Gly Leu Ile Pro Val Leu Glu Thr Val  
 145 150 155 160  
 Cys Leu Glu Asn Arg Val Val Asp Leu Gln Asp Leu Phe Gln Arg Leu  
 165 170 175  
 Thr Phe Asp Thr Thr Cys Thr Phe Val Thr Gly Tyr Asp Pro Gly Cys  
 180 185 190  
 Leu Ser Val Asp Leu Pro Asp Val Pro Phe Ser Lys Ala Leu Asp Asp  
 195 200 205  
 Ala Glu Glu Ala Ile Phe Met Arg His Val Val Pro Glu Lys Ile Trp  
 210 215 220  
 Lys Leu Gln Arg Trp Phe Gly Val Gly Ser Glu Arg Lys Leu Ser Lys  
 225 230 235 240  
 Ala Arg Glu Val Leu Asp Ser Val Ile Gly Arg Tyr Ile Ala Leu Lys  
 245 250 255  
 Arg Gly Glu Met Arg Ser Arg Gly Ile Ser Ile Asp Cys Glu Asn Glu  
 260 265 270  
 Asp Gly Val Asp Leu Leu Thr Ser Tyr Met Thr Val Gly Asp Asp Gly  
 275 280 285  
 Thr Gln Thr His Asp Leu Lys Cys Asp Asp Lys Phe Leu Arg Asp Thr  
 290 295 300  
 Ile Leu Asn Leu Met Ile Ala Gly Arg Asp Thr Thr Ser Ser Ala Leu  
 305 310 315 320  
 Thr Trp Phe Ile Trp Leu Val Ser Thr His Ala Glu Val Glu Lys Arg  
 325 330 335  
 Ile Arg Asp Glu Leu Lys Ser Phe Leu Pro Ala Gly Glu Arg Glu Lys  
 340 345 350  
 Trp Arg Val Phe Gly Val Glu Glu Thr Lys Lys Leu Val Tyr Met His  
 355 360 365  
 Gly Ala Ile Cys Glu Ala Leu Arg Leu Tyr Pro Pro Val Pro Phe Gln  
 370 375 380  
 His Lys Glu Pro Val Glu Pro Asp Ile Leu Pro Ser Gly His Phe Val  
 385 390 395 400  
 Glu Pro Thr Met Lys Val Met Phe Ser Leu Tyr Ala Met Gly Arg Met  
 405 410 415  
 Glu Ser Val Trp Gly Glu Asp Cys Leu Glu Phe Lys Pro Glu Arg Trp  
 420 425 430  
 Ile Ser Asp Arg Gly Ser Ile Lys His Glu Pro Ser Tyr Lys Phe Leu

435 440 445  
 Ala Phe Asn Ala Gly Pro Arg Thr Cys Leu Gly Lys Asp Val Ala Phe  
 450 455 460  
 Ala Gln Val Lys Ala Val Ala Ala Thr Leu Ile His Asn Tyr Gln Val  
 465 470 475 480  
 His Val Ala Asp Gly His Arg Val Leu Pro Asn Cys Ser Ile Ile Leu  
 485 490 495  
 Tyr Met Arg Asn Gly Leu Lys Val Arg Val Ala Asn Arg Trp Ser Ala  
 500 505 510  
 Lys Lys Asn  
 515

&lt;210&gt; 57

&lt;211&gt; 1494

&lt;212&gt; DNA

&lt;213&gt; Sesamum indicum

&lt;220&gt;

&lt;223&gt; SiP168

&lt;400&gt; 57

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 gccaaactct ccaaaacctc cgggcccctg atgcgtctca agctgggaac catgacaaca 240  
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 tccggccaaa agcttgatgc gaaccagggc ctgaggaggg agaagttgcg taatttgcaa 480  
 gactatgtga atgaatgctg cgttagtggc caggctgttg atattgggtg agctgccttt 540  
 acgacgacc ttaatctgat atcgccact cttttctcgg tggattttgc tgatttttgt 600  
 tctggttcgt ctcaagagct taaggatgtt atgagcggga tagcgtctat catcgccga 660  
 ccaaattttg ctgattgttt cctcttctt cggctggttg atccacaggg catcttccgc 720  
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 ctacagacca atgattcggg gacgaaaagt gacatgctga aagagcttct tgaatcaaac 840  
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 gaaattcaag aatcagacat ctcaagactc ccttacctac gagcagtggg gaaagaaagt 1080  
 ttcaggcttc accctgcaac tcctttatcg gtacctaca aggccgacga ggaagcagaa 1140  
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 gactatgatt ggaaacttga aggagggtcg aaaactgaag aaatggacat gagtgaagg 1440  
 ttcgccctca ccctgcaaaa agccattcct ctcaaggcac ttccagttaa aatt 1494

&lt;210&gt; 58

&lt;211&gt; 498

&lt;212&gt; PRT

&lt;213&gt; Sesamum indicum

&lt;220&gt;

&lt;223&gt; SiP168

&lt;400&gt; 58

Met Asp Leu Leu Leu Ser Leu Val Leu Leu Leu Cys Ser Ala Ala Cys  
 1 5 10 15

Ile Trp Phe Leu Arg Val Val Leu Lys Pro Asn Pro Gly Pro Arg Lys  
 20 25 30

Ser Ala Asn Leu Pro Pro Gly Pro Lys Pro Leu Pro Ile Ile Gly Asn  
 35 40 45

Ile Leu Glu Leu Gly Glu Lys Pro His Gln Ser Leu Ala Lys Leu Ser  
 50 55 60

Lys Thr Tyr Gly Pro Leu Met Arg Leu Lys Leu Gly Thr Met Thr Thr  
 65 70 75 80

Val Val Val Ser Ser Pro Glu Ile Ser Arg Ile Val Leu Gln Gln Tyr  
 85 90 95

Asp Gln Val Phe Ser Ser Arg Thr His Ala Asp Ala Ile Arg Ala Leu  
 100 105 110

Asp His His Lys His Ser Val Ala Trp Ile Pro Ala Asp Asn Gln Trp  
 115 120 125

Arg Lys Ile Arg Lys Leu Cys Lys Glu Lys Met Phe Ser Gly Gln Lys  
 130 135 140

Leu Asp Ala Asn Gln Gly Leu Arg Arg Glu Lys Leu Arg Asn Leu Gln  
 145 150 155 160

Asp Tyr Val Asn Glu Cys Cys Val Ser Gly Gln Val Val Asp Ile Gly  
 165 170 175

Val Ala Ala Phe Thr Thr Thr Leu Asn Leu Ile Ser Ala Thr Leu Phe  
 180 185 190

Ser Val Asp Phe Ala Asp Phe Gly Ser Gly Ser Ser Gln Glu Leu Lys  
 195 200 205

Asp Val Met Ser Gly Ile Ala Ser Ile Ile Gly Arg Pro Asn Phe Ala  
 210 215 220

Asp Cys Phe Pro Leu Leu Arg Leu Val Asp Pro Gln Gly Ile Phe Arg  
 225 230 235 240

Gln Thr Thr Leu His Phe Asn Lys Cys Phe Lys Ile Phe Asp Glu Ile  
 245 250 255

Ile Arg Gln Arg Leu Gln Thr Asn Asp Ser Gly Thr Lys Ser Asp Met  
 260 265 270

Leu Lys Glu Leu Leu Glu Ile Asn Gln Lys Asp Glu Ser Glu Leu Ser  
 275 280 285  
 Phe Asp Glu Ile Lys His Leu Leu Leu Asp Leu Leu Val Ala Gly Thr  
 290 295 300  
 Asp Thr Thr Ser Val Thr Val Glu Trp Ala Met Thr Glu Leu Val Arg  
 305 310 315 320  
 His Pro Glu Lys Met Ser Lys Ala Arg Asn Glu Leu Arg Asn Val Val  
 325 330 335  
 Gly Leu Asn Lys Glu Ile Gln Glu Ser Asp Ile Ser Arg Leu Pro Tyr  
 340 345 350  
 Leu Arg Ala Val Val Lys Glu Ser Phe Arg Leu His Pro Ala Thr Pro  
 355 360 365  
 Leu Ser Val Pro His Lys Ala Asp Glu Glu Ala Glu Ile Asn Gly Tyr  
 370 375 380  
 Ile Val Pro Lys Gly Ala Gln Val Leu Met Asn Val Trp Ala Ile Gly  
 385 390 395 400  
 Arg Asp Ser Ser Ile Trp Arg Asn Pro Asp Val Phe Met Pro Glu Arg  
 405 410 415  
 Phe Leu Glu Thr Glu Ile Asp Val Arg Gly Gln His Phe Glu Leu Leu  
 420 425 430  
 Pro Phe Gly Gly Gly Arg Arg Ile Cys Val Gly Leu Pro Leu Ala Tyr  
 435 440 445  
 Arg Met Ile His Leu Val Leu Ala Thr Phe Ile Ser Asp Tyr Asp Trp  
 450 455 460  
 Lys Leu Glu Gly Gly Leu Lys Thr Glu Glu Met Asp Met Ser Glu Lys  
 465 470 475 480  
 Phe Gly Leu Thr Leu Gln Lys Ala Ile Pro Leu Lys Ala Leu Pro Val  
 485 490 495  
 Lys Ile

<210> 59  
 <211> 1545  
 <212> DNA  
 <213> Sesamum indicum

<220>  
 <223> SiP236

<400> 59  
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&lt;210&gt; 60

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Sesamum indicum

&lt;220&gt;

&lt;223&gt; SiP236

&lt;400&gt; 60

Met Ala Asn Pro Ile Asp Phe Leu Leu Ser Pro Thr Pro Tyr Val Ala  
1 5 10 15

Thr Thr Leu Leu Tyr Val Leu Phe Ser Val Leu Ile Val Arg Phe Leu  
20 25 30

Ser Arg Lys Leu Leu Gly Lys Lys Arg Tyr His Pro Ile Gly Gly Thr  
35 40 45

Val Phe Asn Gln Leu Leu Asn Phe Tyr Arg Leu His Asp Tyr Met Ala  
50 55 60

Asp Leu Ala Gly Lys Tyr Lys Thr Tyr Arg Leu Ile Ala Pro Phe Arg  
65 70 75 80

Thr Glu Val Tyr Thr Ser Asp Pro Ala Asn Val Glu His Met Leu Lys  
85 90 95

Thr Asn Phe Glu Ser Tyr Gly Lys Gly Pro Tyr Asn Cys Ser Ile Leu  
100 105 110

Gly Asp Leu Phe Gly Glu Gly-Ile Phe Ala Ile Asp Gly His Lys Trp

115 120 125  
 Arg Glu Gln Arg Lys Val Ser Ser Leu Glu Phe Ser Thr Arg Val Leu  
 130 135 140  
 Arg Asp Tyr Ser Ser Ile Val Phe Arg Lys Asn Ala Val Arg Leu Ala  
 145 150 155 160  
 Lys Ile Leu Ser Gly Ala Ala Thr Ser Asn Gln Pro Val Asp Ile Gln  
 165 170 175  
 Asp Leu Phe Met Lys Ser Thr Phe Asp Ser Ile Ser Glu Val Ala Leu  
 180 185 190  
 Gly Val Glu Leu Asp Ser Leu Gly Gly Ser Asn Glu Glu Gly Ala Lys  
 195 200 205  
 Phe Ser Ile Ala Ala Asp Asp Val Ser Met Arg Thr Leu Trp Arg Tyr  
 210 215 220  
 Val Asp Val Leu Trp Lys Leu Lys Arg Ala Leu Asn Val Gly Ser Glu  
 225 230 235 240  
 Ala Lys Leu Lys Lys Ser Leu Gln Val Val Asp Glu Phe Val Tyr Lys  
 245 250 255  
 Leu Ile His Ser Arg Thr Gln Gln Met Asn Met Pro Gly Asn Asp Ser  
 260 265 270  
 Val Met Gln Leu Lys Lys Asp Asp Ile Leu Ser Arg Phe Leu Gln Leu  
 275 280 285  
 Thr Glu Ala Thr Pro Lys Tyr Leu Arg Asp Ile Thr Ile Ser Phe Ile  
 290 295 300  
 Val Ala Gly Lys Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Ile Tyr  
 305 310 315 320  
 Met Leu Cys Lys Tyr Pro His Val Gln Glu Lys Val Glu Gln Glu Ile  
 325 330 335  
 Lys Asp Ala Thr Gly Cys Lys Glu Val Ala Asp Ile Ser Glu Phe Ser  
 340 345 350  
 Ala Cys Val Thr Glu Glu Ala Leu Gly Lys Met His Tyr Leu His Ala  
 355 360 365  
 Ala Leu Thr Glu Thr Leu Arg Ile Tyr Pro Ala Val Ala Val Asp Ala  
 370 375 380  
 Lys Gln Cys Leu Cys Asp Asp Ile Met Pro Asp Gly Phe Ser Val Lys  
 385 390 395 400  
 Lys Gly Asp Met Val Ala Tyr Gln Pro Tyr Ala Met Gly Arg Met Lys  
 405 410 415  
 Ser Ile Trp Gly Asn Asp Ala Glu Glu Phe Lys Pro Glu Arg Trp Leu

420                      425                      430  
 Asp Lys Asn Gly Cys Phe Gln Gln Ala Ser Pro Phe Lys Phe Thr Ala  
          435                      440                      445  
 Phe Gln Ala Gly Pro Arg Leu Cys Leu Gly Lys Glu Phe Ala Tyr Arg  
          450                      455                      460  
 Gln Met Lys Ile Phe Ser Ala Ile Leu Leu Arg Phe Phe Thr Met Lys  
          465                      470                      475                      480  
 Leu Ser Asp Glu Arg Lys Thr Val Asn Tyr Arg Pro Met Leu Thr Leu  
                  485                      490                      495  
 Leu Ile Asp Gly Gly Leu Ile Val Arg Pro Phe His Arg Met Asp Glu  
                  500                      505                      510  
 Lys Thr Ala  
          515

&lt;210&gt; 61

&lt;211&gt; 34

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, Bam-SST-FW2

&lt;400&gt; 61

tggatcccaa ctcatagagt actcaaaaac gctt

34

&lt;210&gt; 62

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, SiP189-Nco-RV

&lt;400&gt; 62

gcaaagtatc aaccatggtg ttct

24

&lt;210&gt; 63

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, GR-SST-RV1

<400> 63  
cacatgaacg agacgaactg ggttttg 27

<210> 64  
<211> 506  
<212> PRT  
<213> Sesamum radiatum

<220>  
<223> SrSiP189

<400> 64  
Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile  
1 5 10 15

Phe Met Val Tyr Arg Ile Leu Ser Asn Ser Gln Glu Lys Ser Ser Leu  
20 25 30

Ile Lys Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Val Ile Gly His  
35 40 45

Val His Leu Met Lys Asn Leu Leu His Arg Thr Leu Tyr Asp Phe Ser  
50 55 60

Gln Lys Leu Gly Pro Ile Phe Ser Leu Arg Phe Gly Thr Arg Leu Val  
65 70 75 80

Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr  
85 90 95

Asp Ile Val Leu Ala Asn Arg Pro Gln Pro Ser Val Asp Arg Arg Ser  
100 105 110

Leu Gly Phe Ser Thr Thr Ser Val Ile Gly Ala Pro Tyr Gly Asp His  
115 120 125

Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr  
130 135 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Leu Asp Glu Arg Asp Arg Met  
145 150 155 160

Ile Ser Ser Leu Tyr Lys Ile Ser Ser Ala Gly Phe Ala Lys Val Asn  
165 170 175

Leu Glu Thr Lys Ile Val Glu Leu Thr Phe Asn Asn Ile Met Arg Met  
180 185 190

Val Ala Gly Lys Arg Tyr Tyr Gly Glu Glu Ala Glu Asp Asp Glu Glu  
195 200 205

Ala Lys Arg Phe Arg Asp Leu Thr Lys Glu Ala Leu Glu Leu Thr Ser  
210 215 220

Ala Ser Asn Pro Gly Glu Ile Phe Pro Ile Leu Arg Trp Leu Gly Phe  
 225 230 235 240  
 Asn Gly Leu Glu Lys Lys Leu Ala Val His Ala Arg Lys Thr Asp Glu  
 245 250 255  
 Phe Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn  
 260 265 270  
 Thr Met Val Asp His Leu Leu Ser Leu Gln Glu Ser Gln Pro Glu Tyr  
 275 280 285  
 Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Val Ala Leu Ile Ile Ala  
 290 295 300  
 Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Ile  
 305 310 315 320  
 Leu Asn His Pro Gln Val Leu Glu Lys Ala Arg Lys Glu Leu Asp Thr  
 325 330 335  
 Leu Val Gly His Glu Arg Met Val Asp Glu His Asp Leu Pro Lys Leu  
 340 345 350  
 Arg Tyr Leu His Cys Ile Val Leu Glu Thr Leu Arg Leu Phe Pro Ser  
 355 360 365  
 Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Lys Ile Gly  
 370 375 380  
 Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Leu Val Asn Ala Trp Ala  
 385 390 395 400  
 Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Leu Ser Phe Lys Pro  
 405 410 415  
 Asp Arg Phe Glu Thr Met Glu Val Glu Thr His Lys Leu Leu Pro Phe  
 420 425 430  
 Gly Met Gly Arg Arg Ala Cys Pro Gly Ala Gly Leu Ala Gln Lys Phe  
 435 440 445  
 Val Gly Leu Ala Leu Gly Ser Leu Ile Gln Cys Phe Glu Trp Glu Arg  
 450 455 460  
 Met Ser Ala Glu Lys Ile Asp Leu Asn Glu Gly Ser Gly Ile Thr Leu  
 465 470 475 480  
 Pro Lys Ala Lys Thr Leu Glu Ala Met Cys Lys Pro Arg His Ile Met  
 485 490 495  
 Glu Arg Val Leu Arg Gln Val Ser Asn Val  
 500 505

<211> 1518  
 <212> DNA  
 <213> *Sesamum radiatum*

<220>  
 <223> SrSiP189

<400> 65  
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 tacgacttct cccagaaact gggacccata ttttccctcc ggttcggcac ccgcctcgtg 240  
 gtagtggtgt cctcctctct cctggtcgag gaatgtttca ccaagtacga cattgtcttg 300  
 gccaacggcc ctcagccctc tgcgaccgg cgctcactcg ggttcagcac caccagcgta 360  
 atcggcgccc cgtacgggga ccattggcgc aacctgcgaa agttgtgcga tcttgaagta 420  
 ttgccccga cccgtctcgc ctggttttta tccatcaggc ttgacgagag ggaccgcatg 480  
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 gaggaggcgg aggcagacga ggaggcgaag aggttcaggg acctgacgaa ggaggctttg 660  
 gaggttgacga gcgtttccaa tctgtgtgag atatttccaa tattgcggtg gcttgggttc 720  
 aatgggttgg agaagaagct ggctgttcac gcgcggaaga cggatgagtt catgcaaggg 780  
 ctgctggacg aacaccgacg gggcgagcgc cagaacacca tggttgatca ttgtctttcg 840  
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 ctaaatcatc cccaagtact tgaagggtt agaaaagaac tggacactct agtaggacac 1020  
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 tgtaaaattg ggggatacaa tgtccccaag gggacaatga tactgggtga tgcttgggca 1200  
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 acaatggaag tggagacaca caagctgttg ccgttcggga tgggcaggag agcgtgtccc 1320  
 ggagctggat tggcgagaa gtttggggg ttggctttgg ggtcgtgat tcagtgtttc 1380  
 gattgggaga gaatgagtc ggagaaaatt gacttgaacg aaggttcttg gataaccttg 1440  
 cctaaagcta agacgttga agccatgtgc aaacctagac atatcatgga gagagttctt 1500  
 cgtcagggtt cgaacgtc 1518

<210> 66  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, NtUBQ-FW

<400> 66  
 ggaatgcaga tcttcgtcaa

20

<210> 67  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially

## Synthesized Primer Sequence, NtUBQ-RW

<400> 67  
cctagaaacc accacgga

18

<210> 68  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, SiP189-bam-FW

<400> 68  
ttttcagcca acatggaagc tgaa

24

<210> 69  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, SiP189-nco-RV

<400> 69  
gcaaagtatc aacctggtg ttct

24

<210> 70  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, STAR-LF1

<400> 70  
acgaagtat gcggccaatt aacct

25

<210> 71  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, STAR-LR1

<400> 71  
ccacctgacg tcgcgcccta atacg

25

<210> 72  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, M13-47(F)

<400> 72  
 cgccagggtt ttcccgatca cgac

24

<210> 73  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Artificially  
 Synthesized Primer Sequence, RV-M(R)

<400> 73  
 gagcgataa caatttcaca cagg

24

<210> 74  
 <211> 3069  
 <212> DNA  
 <213> Sesamun indium

<400> 74  
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 caatgaaatt gacagatgac gtctagtgtg gtgtgaatgt gtgatatttt tgcagaatat 180  
 tgtaaaagag ggttcaccaa atctcactag tttgtgacta attgactatt tttgcagaaa 240  
 attcgtatatt agtatagggt cttggtcaaa ttaattaatt atataacaaa tgtgatatat 300  
 ttaatttggtt attaatTTTT ttatatttTgt tgtgtaatta gttaggattt tatataagaa 360  
 tttgaaaaaa tgagatgttt ttttgtaaat caaattacac aatatcatgt attgggtttt 420  
 tcgtcctgaa gtcgcttgaa aattgattag atcggcggac ttgaacagac gagtgaatgg 480  
 acatgattta aaattttaag gataaatata tatagtatca gttatcaaaa taaaaaattt 540  
 ccttcaaaat catggtcctt ttaagatag ttttttgagt aatgtggcac cataattccc 600  
 aagcactaga agtgcaattg taaatccaac ggtacctagt ttaattgata aaattaaagt 660  
 ccaaaaattt tccctgagaaa ccaattcgag caagggtaca tcaaagggtgc caccaggagg 720  
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 taaaaagatt caaatggctt agagtcgaga aaaagactaa gtagaccatt agggaagccc 840  
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 ggattcccta gctctgaaag aattaatatt gtccaagaa tctaaggcta catagtagaa 960  
 atgaaaacaa agcgaattta aatttgaagc cagcatgatt gaattttttt tttttttttc 1020  
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 ggggatggaa cacaaaattt taggcatttt ttttcttttt tttttttgtc aaaaatgtct 1440

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gaaaaatttg tctaaaattg aatttaatta aatttaaatt aattatataa taaatataat 2640
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tcctacaaat tctgcagact atgaaaacga catcaaccaa ccaatatcca ctctctatat 3000
aaatagcatc acttcactag caatttctca tcaactcata gactactcaa aaacgctttt 3060
tcagccaac 3069

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&lt;210&gt; 75

&lt;211&gt; 29

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, gSST-FW1

&lt;400&gt; 75

aatgaaattg acagatgacg tctagtgtg

29

&lt;210&gt; 76

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Artificially  
Synthesized Primer Sequence, gSST-RV2

&lt;400&gt; 76

ctgcgaatta gaaagaattc tgtaaaccat

30

&lt;210&gt; 77

&lt;211&gt; 2815

&lt;212&gt; DNA

<213> *Sesamum radiatum*

&lt;400&gt; 177

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ggtaaaatct aatttataga gtaaatatga tgtatttatt ttgtgattga ttacttttat 180
atttatgtta taattagtta taatttgata aagtgatgata ttttttataa attagattac 240
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gccactataa agaaaattga cccaagaga tacaagtatc tttagagtcga gaagaagact 660
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&lt;210&gt; 78

&lt;211&gt; 507

&lt;212&gt; PRT

&lt;213&gt; Sesumum alatum

&lt;400&gt; 78

Met Glu Ala Glu Met Leu Tyr Ser Ala Leu Ala Leu Thr Phe Ala Ile  
 1 5 10 15

Ile Met Val His Arg Ile Leu Ser Asn Ser Gln Asn Lys Arg Ser Leu  
 20 25 30

Ile Asn Leu Pro Pro Ser Pro Pro Gly Trp Leu Pro Ile Ile Gly His  
 35 40 45

Leu His Leu Ile Lys Asn Pro Leu His Arg Thr Leu Tyr Asp Cys Ser  
 50 55 60

Gln Lys Leu Gly Ser Ile Phe Ser Val Trp Phe Gly Ser Arg Leu Val  
 65 70 75 80

Val Val Val Ser Ser Ser Ser Leu Val Glu Glu Cys Phe Thr Lys Tyr  
 85 90 95

Asp Ile Val Leu Ala Asn Arg Pro Asp Leu His Leu Asp Leu Arg Ser  
 100 105 110

Leu Gly Ala Ser Thr Ile Ser Val Ile Gly Ala Pro Tyr Gly Asp His  
 115 120 125

Trp Arg Asn Leu Arg Lys Leu Cys Asp Leu Glu Val Phe Ala Pro Thr  
 130 135 140

Arg Leu Ala Ser Phe Leu Ser Ile Arg Arg Asp Glu Arg Asp Arg Met  
 145 150 155 160

Ile Ser Gly Leu Tyr Lys Ile Ser Ser Ala Gly Leu Ala Lys Val Asn  
 165 170 175

Leu Glu Ala Lys Ile Ala Glu Leu Thr Phe Asn Asn Leu Met Arg Met  
 180 185 190

Leu Ala Gly Lys Ile Tyr Tyr Gly Glu Glu Ala Glu Asp Glu Glu Glu  
 195 200 205

Ala Lys Arg Phe Arg Asp Met Thr Lys Glu Ala Leu Glu Leu Met Asn  
 210 215 220

Thr Phe Asn Leu Ala Glu Ile Phe Pro Ile Leu Arg Trp Ile Gly Cys  
 225 230 235 240

Asn Gly Phe Glu Lys Gln Leu Pro Val His Ser Arg Lys Thr Asp Glu  
 245 250 255

Ile Met Gln Gly Leu Leu Asp Glu His Arg Arg Gly Glu Arg Gln Asn  
 260 265 270

Thr Met Val Gly His Leu Leu Ser Leu Gln Glu Ser Gln Pro Asp Tyr  
 275 280 285

Tyr Thr Asp Glu Ile Ile Thr Gly Leu Ile Ile Ser Leu Ile Ile Ala  
 290 295 300  
 Gly Thr Asp Ala Ser Val Val Thr Thr Glu Trp Ala Met Ser Leu Leu  
 305 310 315 320  
 Leu Asn His Pro Lys Val Leu Glu Lys Ala Arg Gln Glu Met Asp Thr  
 325 330 335  
 Leu Val Gly His Glu Arg Met Val Glu Glu Asp Asp Leu Pro Lys Leu  
 340 345 350  
 Arg Tyr Leu His Tyr Ile Ile Leu Glu Thr Leu Arg Leu Phe Pro Ser  
 355 360 365  
 Val Pro Thr Leu Val Pro His Glu Pro Ser Glu Asp Cys Asn Ile Gly  
 370 375 380  
 Gly Tyr Asn Val Pro Lys Gly Thr Met Ile Ile Val Asn Ala Trp Ala  
 385 390 395 400  
 Ile His Arg Asp Pro Lys Val Trp Asp Asp Pro Met Ser Phe Lys Pro  
 405 410 415  
 Asp Arg Phe Glu Thr Leu Glu Val Glu Thr His Lys Leu Leu Pro Phe  
 420 425 430  
 Gly Met Gly Arg Arg Gly Cys Pro Gly Ala Gly Leu Ala Lys Lys Phe  
 435 440 445  
 Val Gly Leu Ala Leu Ala Ser Leu Ile Gln Cys Phe Asp Trp Glu Arg  
 450 455 460  
 Ile Ser Ala Glu Lys Ile Asp Leu Lys Glu Gly Ala Ser Arg Ile Thr  
 465 470 475 480  
 Leu Pro Lys Ala Thr Thr Leu Glu Ala Met Cys Lys Pro Arg His Val  
 485 490 495  
 Met Glu Lys Val Leu Arg Gln Val Ser Asn Val  
 500 505

&lt;210&gt; 79

&lt;211&gt; 1524

&lt;212&gt; DNA

&lt;213&gt; Sesumum alatum

&lt;400&gt; 79

atggaagctg aaatgctata ttcagctctc gctctcacct tcgccataat catggttcac 60  
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 ggttggtgc cgattatcgg ccaccttcac ctcataaaaa atccactcca tagaacacta 180  
 tacgactgct cccagaaact gggatccata ttctccgtct ggttcgggtc ccgcctcgtg 240  
 gtggtggtgt cctcctcctc cctggtggag gaatgtttca ccaagtacga cattgtcttg 300  
 gccaacgcc ctgacctcca tctggacctg cgatcactcg gggccagcac catcagcgta 360  
 atcggggccc cttacgggga ccactggcgc aacctgcgaa agttgtgcga tcttgaagta 420  
 ttcgccccga cccgtctcgc ctcttctta tccatcagac gagacgagag ggaccgcatg 480

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